

Mon Sep 8 07:48:44 2003

us-10-08

FT DOMAIN 101 195 PLASTOCYANIN-LIKE 1.
FT DOMAIN 245 346 PLASTOCYANIN-LIKE 2.
FT DOMAIN 368 387 4 X 5 AA TANDEM REPEATS OF A-A-S-A-P.
FT REPEAT 368 372 1.
FT REPEAT 373 377 2.
FT REPEAT 378 382 3.
FT REPEAT 383 387 4.
SQ SEQUENCE 392 AA; 40954 MW; A4707CC87B923C97 CRC64;

Query Match 52.8%; Score 1386; DB 1; Length 392;
Best Local Similarity 69.5%; Pred. No. 4.4e-90;
Matches 264; Conservative 44; Mismatches 66; Indels 6; Gaps 3;

QY 11 LICALSALMLSGCSNQADKAAQPKSSTVDAAKTA-NADNAASQEHQGLPVIDAIVTHA 69
Db 9 MIASLPALACG---GEQAAQAPAEPTPAASAAEAASAAQATAETPAGELEFVIDAVTTHA 64
QY 70 PEVPPPVD RDHPAKVVKMETVEKVMRLADGVEYQFWTFGGOVPGQMIRVREGDTIEVQF 129
Db 65 PEVPPAIDRDYPKVRVKMETVEKTMKMDGVEYRYWTFDGDVPGRMIRVREGDTVEVEF 124
QY 130 SNHPDSKMPHNVDFAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGMHI.189
Db 125 SNNPSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPGLYIYHCAVAPVGMHI 184
QY 190 ANGMYGLILVEPKGLPKVDKEYVVMQGDFTYTKGKYGEQGLQPFDMKAIREDAEYVVFN 249
Db 185 ANGMYGLILVEPKGLPKVDKEYVIVQGDFTYTKGKGAQGLQPFDMKAVAEQPEYVVFN 244
QY 250 GSVGALTGENALKAKVGETVRLFVNGGPNLTSSPHVIGEIPDKVHFEGGKGENHNIQT 309
Db 245 GHVGSAGDNALKAKAGETVRMYVNGGPNLVSSPHVIGEIPDKVYVEGGKLINENVQST 304
QY 310 LIPAGGAAITEFKVDVPGDYVLVDHAI FRAFNKGALGILKVEGEENHEIYSHKQTDVAVYL 369
Db 305 IVPAGGSAIVEFKVDIPGSYTLVDHSIFRAFNKGALGQLKVEGAENPEIMTQKLSDTAYA 364
QY 370 PEGAPQAIDTQEA PKTPAPA 389
Db 365 GSGAASA-PAASAPAASAPA 383

RESULT 2

NIR_RHOSH

ID NIR_RHOSH STANDARD; PRT; 374 AA.
AC Q53239;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Copper-containing nitrite reductase precursor (EC 1.7.2.1) (Cu-NIR).
GN NIKK.
OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2.4.3;
RX MEDLINE=97175533; PubMed=9023188;
RA Tosques I.E., Kwiatkowski A.V., Shi J., Shapleigh J.P.;
RT "Characterization and regulation of the gene encoding nitrite
reductase in Rhodobacter sphaeroides 2.4.3.";
RL J. Bacteriol. 179:1090-1095 (1997).
CC -1- CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferricytochrome c =
nitrite + ferrocycytochrome c.
CC -1- COFACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TYPE
II COPPER; FAD. TYPE I COPPER IS BOUND WITHIN A SINGLE MONOMER,
WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS
OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.
PSEUDOAZURIN IS THE PHYSIOLOGICAL ELECTRON DONOR FOR THE CU-NIR IN
VITRO (BY SIMILARITY).
CC -1- PATHWAY: Nitrate assimilation (denitrification).
CC SUBUNIT: Homotrimer (By similarity).

Doc in 179 -
10

BEST AVAILABLE COPY

Mon Sep 8 07:48:44 2003

34	109	4.2	108	1	C555_CHLTE	Q8kg93	chlorobium
35	109	4.2	1062	1	CERU_MOUSE	Q61147	mus musculus
36	108	4.1	527	1	LAC5_TRAVE	Q12717	trametes ve
37	107.5	4.1	520	1	LAC2_AGABI	Q12542	agaricus bi
38	107.5	4.1	1257	1	CCAA_BACTU	Q45754	bacillus th
39	107.5	4.1	2647	1	FLNA_HUMAN	P21333	homo sapien
40	107	4.1	1654	1	OMPB_RICRI	Q53047	r outer mem
41	106.5	4.1	485	1	IMDH_PYRAB	Q9uy49	pyrococcus
42	106.5	4.1	599	1	LAC2_THACU	Q02075	thanatephor
43	106.5	4.1	642	1	PHSA_STRAT	Q53692	streptomyce
44	105.5	4.0	739	1	PURL_CAUCR	Q9a5f0	caulobacter
45	105	4.0	86	1	C555_CHLLT	P00123	chlorobium

ALIGNMENTS

RESULT 1

ANIA_NEIGO

ID ANIA_NEIGO STANDARD; PRT; 392 AA.

AC Q02219;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Major outer membrane protein Pan 1 precursor.

GN ANIA.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=R10;

RX MEDLINE=93014187; PubMed=1383156;

RA Hoehn G.T., Clark V.L.;

RT "Isolation and nucleotide sequence of the gene (aniA) encoding the

RT major anaerobically induced outer membrane protein of Neisseria

RT gonorrhoeae.";

RL Infect. Immun. 60:4695-4703(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33084 / F62;

RX MEDLINE=93014188; PubMed=1398981;

RA Hoehn G.T., Clark V.L.;

RT "The major anaerobically induced outer membrane protein of Neisseria

RT gonorrhoeae, Pan 1, is a lipoprotein.";

RL Infect. Immun. 60:4704-4708(1992).

CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid

CC anchor. (Probable).

CC -!- INDUCTION: BY ANAEROBIOSIS.

CC -!- SIMILARITY: Contains 2 plastocyanin-like domains.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; M97926; AAA25462.1; -.

DR PIR; A49208; A49208.

DR PDB; 1KBV; 27-FEB-02.

DR PDB; 1KBW; 27-FEB-02.

DR InterPro; IPR001117; Cu-oxidase.

DR InterPro; IPR001287; CuNO2 reductase.

DR Pfam; PF00394; Cu-oxidase; 2.

DR PRINTS; PR00695; CUNO2RDTASE.

DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

KW Repeat; Outer membrane; Lipoprotein; Signal; 3D-structure.

FT SIGNAL 1 18

FT CHAIN 19 392 MAJOR OUTER MEMBRANE PROTEIN PAN 1.

FT LIPID 19 19 N-ACYL DIGLYCERIDE (PROBABLE).

BEST AVAILABLE COPY